

Ile Phe Ser Gln Ser Val Ser Pro Cys Gly Lys Phe Leu Ala Ala Gly

aac aat tac ggg cag att gcc atc ttc agc ttg tcc tct gct ttg agc	437
Asn Asn Tyr Gly Gln Ile Ala Ile Phe Ser Leu Ser Ser Ala Leu Ser	
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tca gaa gcc aaa gag gaa agt aag aag ccg gtg gtg act ttc caa gcc	485
Ser Glu Ala Lys Glu Glu Ser Lys Lys Pro Val Val Thr Phe Gln Ala	
60 65 70	
cat gat ggg ccc gtc tat agc atg gtt tcc acc gat cga cat ctg ctt	533
His Asp Gly Pro Val Tyr Ser Met Val Ser Thr Asp Arg His Leu Leu	
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agt gct ggg gat ggg gag gag aag gcc tgg ctt tgg gcg gag atg ctc	581
Ser Ala Gly Asp Gly Glu Glu Lys Ala Trp Leu Trp Ala Glu Met Leu	
95 100 105	
aag aag ggc tgt aag gag ctg tgg cgt cgt cag cct cca tac agg acc	629
Lys Lys Gly Cys Lys Glu Leu Trp Arg Arg Gln Pro Pro Tyr Arg Thr	
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agc ctg gaa gtg cct gag atc aac gct ttg ctg ctg gtc ccc aag gag	677
Ser Leu Glu Val Pro Glu Ile Asn Ala Leu Leu Leu Val Pro Lys Glu	
125 130 135	
aat tcc ctc atc ctg gct ggg gga gac tgt cag ttg cac act atg gac	725
Asn Ser Leu Ile Leu Ala Gly Gly Asp Cys Gln Leu His Thr Met Asp	
140 145 150	
ctt gaa act ggg act ttc acg agg gtc ctc cgg ggc cac aca gac tac	773
Leu Glu Thr Gly Thr Phe Thr Arg Val Leu Arg Gly His Thr Asp Tyr	
155 160 165 170	
atc cac tgc ctg gca ctg cgg gaa agg agc cca gag gtg ctg tca ggt	821
Ile His Cys Leu Ala Leu Arg Glu Arg Ser Pro Glu Val Leu Ser Gly	
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ggc gag gat gga gct gtt cga ctt tgg gac ctg cgc aca gcc aag gag	869
Gly Glu Asp Gly Ala Val Arg Leu Trp Asp Leu Arg Thr Ala Lys Glu	
190 195 200	
gtc cag acg atc gag gtc tat aag cac gag gag tgc tgc agg ccc cac	917
Val Gln Thr Ile Glu Val Tyr Lys His Glu Glu Cys Ser Arg Pro His	
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Asn Gly Arg Trp Ile Gly Cys Leu Ala Thr Asp Ser Asp Trp Met Val	
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tgt gga ggg ggc cca gcc ctc acc ctc tgg cac ctc cga tcc tcc aca	1013
Cys Gly Gly Gly Pro Ala Leu Thr Leu Trp His Leu Arg Ser Ser Thr	
235 240 245 250	
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Pro Thr Thr Ile Phe Pro Ile Arg Ala Pro Gln Lys His Val Thr Phe	
255 260 265	

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 Val Phe Thr Asn Leu Gly Tyr Arg Ala Phe Ser Leu Ser Phe  
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<213> Homo sapiens

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Ser Pro Cys Gly Lys Phe Leu Ala Ala Gly Asn Asn Tyr Gly Gln Ile  
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Ala Ile Phe Ser Leu Ser Ser Ala Leu Ser Ser Glu Ala Lys Glu Glu  
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Ser Lys Lys Pro Val Val Thr Phe Gln Ala His Asp Gly Pro Val Tyr  
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Ser Met Val Ser Thr Asp Arg His Leu Leu Ser Ala Gly Asp Gly Glu  
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Glu Lys Ala Trp Leu Trp Ala Glu Met Leu Lys Lys Gly Cys Lys Glu  
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Leu Trp Arg Arg Gln Pro Pro Tyr Arg Thr Ser Leu Glu Val Pro Glu  
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Ile Asn Ala Leu Leu Leu Val Pro Lys Glu Asn Ser Leu Ile Leu Ala  
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Gly Gly Asp Cys Gln Leu His Thr Met Asp Leu Glu Thr Gly Thr Phe  
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Thr Arg Val Leu Arg Gly His Thr Asp Tyr Ile His Cys Leu Ala Leu  
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Arg Glu Arg Ser Pro Glu Val Leu Ser Gly Gly Glu Asp Gly Ala Val  
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Arg Leu Trp Asp Leu Arg Thr Ala Lys Glu Val Gln Thr Ile Glu Val  
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Tyr Lys His Glu Glu Cys Ser Arg Pro His Asn Gly Arg Trp Ile Gly  
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 Cys Leu Ala Thr Asp Ser Asp Trp Met Val Cys Gly Gly Gly Pro Ala  
 225 230 235 240  
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 Ile Arg Ala Pro Gln Lys His Val Thr Phe Tyr Gln Asp Leu Val Leu  
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Pro	Pro	Asp	Phe	Asp	Pro	Pro	Trp	Val	Glu	Lys	Ala	Asn	Arg	Thr	Arg	
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Gly	Val	Gly	Lys	Glu	Ala	Ser	Lys	Ala	Leu	Gly	Ala	Lys	Gly	Ser	Cys	
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Lys	Asn	Lys	Tyr	Arg	Pro	Ile	Ser	His	Thr	Pro	Ser	Tyr	Cys	Asp	Glu	
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Met	Ala	Lys	Gly	Asp	Ala	Lys	Leu	Arg	Ala	Leu	Leu	Trp	Thr	Pro		
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cca	cct	acc	ccc	agg	ggt	agc	cac	tcg	ccc	cgc	ccc	agg	gag	gca	cca	1138
Pro	Pro	Thr	Pro	Arg	Gly	Ser	His	Ser	Pro	Arg	Pro	Arg	Glu	Ala	Pro	
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ctg	cga	gcc	att	cac	cca	gct	ggt	ccc	tcc	aag	aca	gag	ccg	ggg	cca	1186
Leu	Arg	Ala	Ile	His	Pro	Ala	Gly	Pro	Ser	Lys	Thr	Glu	Pro	Gly	Pro	
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Ala	Ala	Asp	Ser	Gln	Lys	Leu	Ser	Met	Gly	Gly	Leu	His	Ser	Ser	Arg	
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ccc	ctg	aag	cgg	gga	ctt	tcc	cat	tcc	ctc	acc	cac	ctg	aat	gtc	ccc	1282
Pro	Leu	Lys	Arg	Gly	Leu	Ser	His	Ser	Leu	Thr	His	Leu	Asn	Val	Pro	
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Ser	Thr	Gly	His	Pro	Ala	Thr	Ser	Ala	Pro	His	Thr	Asn	Gly	Pro	Gln	
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Asp	Leu	Arg	Pro	Ser	Thr	Ser	Gly	Val	Thr	Phe	Arg	Ser	Pro	Leu	Val	
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act	tcc	agg	gct	cgc	tca	gtt	agc	att	tca	gtg	cca	tct	acc	cca	cga	1426
Thr	Ser	Arg	Ala	Arg	Ser	Val	Ser	Ile	Ser	Val	Pro	Ser	Thr	Pro	Arg	
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 Pro Pro Asp Phe Asp Pro Pro Trp Val Glu Lys Ala Asn Arg Thr Arg  
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 Gly Val Gly Lys Glu Ala Ser Lys Ala Leu Gly Ala Lys Gly Ser Cys  
 65 70 75 80  
 Glu Thr Thr Pro Ser Arg Gly Ser Thr Pro Thr Leu Thr Pro Arg Lys  
 85 90 95  
 Lys Asn Lys Tyr Arg Pro Ile Ser His Thr Pro Ser Tyr Cys Asp Glu  
 100 105 110  
 Ser Leu Phe Gly Ser Arg Ser Glu Gly Ala Ser Phe Gly Ala Pro Arg  
 115 120 125  
 Met Ala Lys Gly Asp Ala Ala Lys Leu Arg Ala Leu Leu Trp Thr Pro  
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 Pro Pro Thr Pro Arg Gly Ser His Ser Pro Arg Pro Arg Glu Ala Pro  
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 Leu Arg Ala Ile His Pro Ala Gly Pro Ser Lys Thr Glu Pro Gly Pro  
 165 170 175  
 Ala Ala Asp Ser Gln Lys Leu Ser Met Gly Gly Leu His Ser Ser Arg  
 180 185 190

Pro Leu Lys Arg Gly Leu Ser His Ser Leu Thr His Leu Asn Val Pro  
 195 200 205

Ser Thr Gly His Pro Ala Thr Ser Ala Pro His Thr Asn Gly Pro Gln  
 210 215 220

Asp Leu Arg Pro Ser Thr Ser Gly Val Thr Phe Arg Ser Pro Leu Val  
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 Met Cys Thr Thr Met Arg Asp Lys Val Phe Gly Asn Tyr Ile Pro  
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 Val Pro Ala Thr Asp Cys Met Ala Val Ser Thr Phe Trp Ile Ala His  
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 Pro Asn Asn Asn Leu Ile Asn Asn Ala Ala Ala Gly Ser Gln Asp Ala  
 35 40 45  
 gga ata tgg tat tta ttc cac aag gaa cca act ggg gaa tcc agt gga 371  
 Gly Ile Trp Tyr Leu Phe His Lys Glu Pro Thr Gly Glu Ser Ser Gly  
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 Leu Gln Leu Leu Ala Lys Pro Glu Leu Thr Pro Leu Gly Ile Phe Tyr  
 65 70 75  
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Gly Val Lys Thr 100 Thr Asn Ser Ser Ala 105 Ala Asp Pro Arg Glu Tyr Leu 110	
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Cys Leu Asp Asn Ser Ala Arg Phe Arg Pro His Gln Asp Ala Asn Pro 125	
gaa aaa cca cgt gtt gct gct cta att gac agg ctc att gct ttt aaa	611
Glu Lys Pro Arg Val Ala Ala Leu Ile Asp Arg Leu Ile Ala Phe Lys 130 135 140	
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Asn Asn Asp Asn Gly Ala Trp Val Arg Gly Gly Asp Ile Ile Val Gln 145 150 155	
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Asn Ser Ala Phe Ala Asp Asn Gly Ile Gly Leu Thr Phe Ala Ser Asp 160 165 175	
gga agc ttc cca agt gat gaa ggt tcc agc caa gag gta tct gaa tct	755
Gly Ser Phe Pro Ser Asp Glu Gly Ser Ser Gln Glu Val Ser Glu Ser 180 185 190	
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Leu Phe Val Gly Glu Ser Arg Asn Tyr Gly Phe Gln Gly Gly Gln Asn 195 200 205	
aag tat gta ggc act gga gga ata gac cag aag cct cga aca tta ccc	851
Lys Tyr Val Gly Thr Gly Gly Ile Asp Gln Lys Pro Arg Thr Leu Pro 210 215 220	
agg aac agg acg ttc cca att aga ggc ttt cag att tat gat ggg ccc	899
Arg Asn Arg Thr Phe Pro Ile Arg Gly Phe Gln Ile Tyr Asp Gly Pro 225 230 235	
att cat ctc aca agg agc act ttc aaa aaa tat gtg cca act cca gat	947
Ile His Leu Thr Arg Ser Thr Phe Lys Lys Tyr Val Pro Thr Pro Asp 240 245 255	
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Arg Tyr Ser Ser Ala Ile Gly Phe Leu Met Lys Asn Ser Trp Gln Ile 260 265 270	
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Thr Pro Arg Asn Asn Ile Ser Leu Val Lys Phe Gly Pro His Val Ser 275 280 285	
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Leu Asn Val Phe Phe Gly Lys Pro Gly Pro Trp Phe Glu Asp Cys Glu 290 295 300	
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Met Asp Gly Asp Lys Asn Ser Ile Phe His Asp Ile Asp Gly Ser Val 305 310 315	

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Arg Gln Val Val Phe Thr Ser Asp Pro His Lys Ser Tyr Leu Pro Val	
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Gln Phe Gln Ser Pro Asp Lys Ala Glu Ala Gln Arg Gly Asp Pro Ser	
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Val Ile Ser Val Asn Gly Thr Asp Phe Thr Phe Arg Ser Ala Gly Val	
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Leu Leu Leu Val Val Asp Pro Cys Ser Val Pro Phe Arg Leu Thr Glu	
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Lys Thr Val Phe Pro Leu Ala Asp Val Ser Arg Ile Glu Glu Tyr Leu	
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Lys Thr Gly Ile Pro Pro Arg Ser Ile Val Leu Leu Ser Thr Arg Gly	
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Glu Ile Lys Gln Leu Asn Ile Ser His Leu Leu Val Pro Leu Gly Leu	
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 tattgttttg tgtggatttt ttaaagcttt tctgttcacc ctcctgccag gaaaatccca 3397  
 gaaagcttaa tgatacccca aaatgattac acccaggag gaaaaaagg agcgctttct 3457  
 agggtcagaa tctgtggagag aatactcaga aatgaacctc tttaaagcct tgcaggaatg 3517  
 agtcactctt acttaatgaa atgttaaagc caattaaaaa gcatgctgtg atgccagct 3577  
 tccctttcca cagggtgcat gcgtctcctg ctggtgaatc acatgcggca agaggcaact 3637  
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 gtatattgat gaatgagatc ttacctatta aatatgttat tggattatgg ttctgaagg 4057  
 tcattagagt gtgtgtgtgt gtgtgtgtgt gtgtgtgttt tatgacttaa atatctttac 4117  
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<210> 6  
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 <212> PRT  
 <213> Homo sapiens

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 Pro Ala Thr Asp Cys Met Ala Val Ser Thr Phe Trp Ile Ala His Pro  
                   20                  25                  30  
 Asn Asn Asn Leu Ile Asn Asn Ala Ala Ala Gly Ser Gln Asp Ala Gly  
           35                  40                  45  
 Ile Trp Tyr Leu Phe His Lys Glu Pro Thr Gly Glu Ser Ser Gly Leu  
   50                  55                  60  
 Gln Leu Leu Ala Lys Pro Glu Leu Thr Pro Leu Gly Ile Phe Tyr Asn  
   65                  70                  75                  80  
 Asn Arg Val His Ser Asn Phe Lys Ala Gly Leu Phe Ile Asp Lys Gly  
                   85                  90                  95  
 Val Lys Thr Thr Asn Ser Ser Ala Ala Asp Pro Arg Glu Tyr Leu Cys  
           100                  105                  110  
 Leu Asp Asn Ser Ala Arg Phe Arg Pro His Gln Asp Ala Asn Pro Glu  
   115                  120                  125  
 Lys Pro Arg Val Ala Ala Leu Ile Asp Arg Leu Ile Ala Phe Lys Asn  
   130                  135                  140  
 Asn Asp Asn Gly Ala Trp Val Arg Gly Gly Asp Ile Ile Val Gln Asn  
   145                  150                  155                  160  
 Ser Ala Phe Ala Asp Asn Gly Ile Gly Leu Thr Phe Ala Ser Asp Gly  
           165                  170                  175  
 Ser Phe Pro Ser Asp Glu Gly Ser Ser Gln Glu Val Ser Glu Ser Leu  
           180                  185                  190  
 Phe Val Gly Glu Ser Arg Asn Tyr Gly Phe Gln Gly Gly Gln Asn Lys  
   195                  200                  205  
 Tyr Val Gly Thr Gly Gly Ile Asp Gln Lys Pro Arg Thr Leu Pro Arg  
   210                  215                  220  
 Asn Arg Thr Phe Pro Ile Arg Gly Phe Gln Ile Tyr Asp Gly Pro Ile  
   225                  230                  235                  240  
 His Leu Thr Arg Ser Thr Phe Lys Lys Tyr Val Pro Thr Pro Asp Arg  
           245                  250                  255  
 Tyr Ser Ser Ala Ile Gly Phe Leu Met Lys Asn Ser Trp Gln Ile Thr  
           260                  265                  270

Pro	Arg	Asn	Asn	Ile	Ser	Leu	Val	Lys	Phe	Gly	Pro	His	Val	Ser	Leu	275	280	285
Asn	Val	Phe	Phe	Gly	Lys	Pro	Gly	Pro	Trp	Phe	Glu	Asp	Cys	Glu	Met	290	295	300
Asp	Gly	Asp	Lys	Asn	Ser	Ile	Phe	His	Asp	Ile	Asp	Gly	Ser	Val	Thr	305	310	315
Gly	Tyr	Lys	Asp	Ala	Tyr	Val	Gly	Arg	Met	Asp	Asn	Tyr	Leu	Ile	Arg	325	330	335
His	Pro	Ser	Cys	Val	Asn	Val	Ser	Lys	Trp	Asn	Ala	Val	Ile	Cys	Ser	340	345	350
Gly	Thr	Tyr	Ala	Gln	Val	Tyr	Val	Gln	Thr	Trp	Ser	Thr	Gln	Asn	Leu	355	360	365
Ser	Met	Thr	Ile	Thr	Arg	Asp	Glu	Tyr	Pro	Ser	Asn	Pro	Met	Val	Leu	370	375	380
Arg	Gly	Ile	Asn	Gln	Lys	Ala	Ala	Phe	Pro	Gln	Tyr	Gln	Pro	Val	Val	385	390	395
Met	Leu	Glu	Lys	Gly	Tyr	Thr	Ile	His	Trp	Asn	Gly	Pro	Ala	Pro	Arg	405	410	415
Thr	Thr	Phe	Leu	Tyr	Leu	Val	Asn	Phe	Asn	Lys	Asn	Asp	Trp	Ile	Arg	420	425	430
Val	Gly	Leu	Cys	Tyr	Pro	Ser	Asn	Thr	Ser	Phe	Gln	Val	Thr	Phe	Gly	435	440	445
Tyr	Leu	Gln	Arg	Gln	Asn	Gly	Ser	Leu	Ser	Lys	Ile	Glu	Glu	Tyr	Glu	450	455	460
Pro	Val	His	Ser	Leu	Glu	Glu	Leu	Gln	Arg	Lys	Gln	Ser	Glu	Arg	Lys	465	470	475
Phe	Tyr	Phe	Asp	Ser	Ser	Thr	Gly	Leu	Leu	Phe	Leu	Tyr	Leu	Lys	Ala	485	490	495
Lys	Ser	His	Arg	His	Gly	His	Ser	Tyr	Cys	Ser	Ser	Gln	Gly	Cys	Glu	500	505	510
Arg	Val	Lys	Ile	Gln	Ala	Ala	Thr	Asp	Ser	Lys	Asp	Ile	Ser	Asn	Cys	515	520	525
Met	Ala	Lys	Ala	Tyr	Pro	Gln	Tyr	Tyr	Arg	Lys	Pro	Ser	Val	Val	Lys	530	535	540
Arg	Met	Pro	Ala	Met	Leu	Thr	Gly	Leu	Cys	Gln	Gly	Cys	Gly	Thr	Arg	545	550	555
Gln	Val	Val	Phe	Thr	Ser	Asp	Pro	His	Lys	Ser	Tyr	Leu	Pro	Val	Gln	565	570	575

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<210> 7
<211> 1545
<212> DNA
<213> Homo sapiens
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gacacggctc ccaggcctct gaccctgct ctaattggga cctgctgtgt ggccctccct 180
tgcttaccag ctgacaggaa cccttctca cccccagggt ggacacgccg tttccaaggc 240
ctcatggctt cctttttctt ggttactgcc tcgggctccc tgggagagat ctctttggtg 300
ccgaaaaccg gaacgggaag cctcagcacc ctggccccc atg  ccc  ctc  gtg  ggg      355
              Met  Pro  Leu  Val  Gly
                  1          5

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cag ggt ggg tat acc ctg tac acc ctc ctg gtt tgg gct gag ggc att	403
Gln Gly Gly Tyr Thr Leu Tyr Thr Leu Leu Val Trp Ala Glu Gly Ile	
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agg ggt acc ggg cgt ctt tgg ggt ggc att agc ccc cga gtt gct ttg	451
Arg Gly Thr Gly Arg Leu Trp Gly Gly Ile Ser Pro Arg Val Ala Leu	
25 30 35	
gaa act gtc ata ctt tct tct gtc tta gaa ctc aga atc caa gaa atg	499
Glu Thr Val Ile Leu Ser Ser Val Leu Glu Leu Arg Ile Gln Glu Met	
40 45 50	
gca tcc atg ggg ata ggc aac cag cca ttc atg gat gtc aag ccc aga	547
Ala Ser Met Gly Ile Gly Asn Gln Pro Phe Met Asp Val Lys Pro Arg	
55 60 65	
gac cgg acc cct gac tgt gca gtg ata agc gac ggg gct ccc aaa tgt	595
Asp Arg Thr Pro Asp Cys Ala Val Ile Ser Asp Gly Ala Pro Lys Cys	
70 75 80 85	
gca gtg atg agc gac cgg gtc ccc gac agc atc gtc aag ggc aca ggt	643
Ala Val Met Ser Asp Arg Val Pro Asp Ser Ile Val Lys Gly Thr Gly	
90 95 100	
acg gtg gct cgg tcc cgc cct cac tca ccc tgc aga ggg cac tgg gcc	691
Thr Val Ala Arg Ser Arg Pro His Ser Pro Cys Arg Gly His Trp Ala	
105 110 115	
tgt cat caa ggg cat ggg tac ggc ggc atc ggc ccc acc ctc act cgc	739
Cys His Gln Gly His Gly Tyr Gly Gly Ile Gly Pro Thr Leu Thr Arg	
120 125 130	
cca cag agt gca cca ggc ctg tcg tca agg aca cgg gta cgg tgg cct	787
Pro Gln Ser Ala Pro Gly Leu Ser Ser Arg Thr Arg Val Arg Trp Pro	
135 140 145	
cgg ccc cgc cct cac tca tcc tgc aga ggg cac tgg gcc agt ggc cga	835
Arg Pro Arg Pro His Ser Ser Cys Arg Gly His Trp Ala Ser Gly Arg	
150 155 160 165	
cat ggt ggg ttg gat ggg cat gac tgc agt ggc aaa gcc tgg tcg gcc	883
His Gly Gly Leu Asp Gly His Asp Cys Ser Gly Lys Ala Trp Ser Ala	
170 175 180	
ttt cag acg gct ctg atc cca ttc ccg aac ctg ggc tgc act tca gga	931
Phe Gln Thr Ala Leu Ile Pro Phe Pro Asn Leu Gly Cys Thr Ser Gly	
185 190 195	
gcg gaa gcc agc ctg acg tgc ttt ctg tcc ctt tcc aga gtc aca aat	979
Ala Glu Ala Ser Leu Thr Cys Phe Leu Ser Leu Ser Arg Val Thr Asn	
200 205 210	
gag agg gtc cac agc ggt gtc ctc ctc tgaccacgcc gcccccttca	1026
Glu Arg Val His Ser Gly Val Leu Leu	
215 220	
agcgaccaca ctccaccatc tcagacagca gcacctctc ttctagcagc cagtcctcct	1086

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Pro Arg Val Ala Leu Glu Thr Val Ile Leu Ser Ser Val Leu Glu Leu  
35 40 45  
Arg Ile Gln Glu Met Ala Ser Met Gly Ile Gly Asn Gln Pro Phe Met  
50 55 60  
Asp Val Lys Pro Arg Asp Arg Thr Pro Asp Cys Ala Val Ile Ser Asp  
65 70 75 80  
Gly Ala Pro Lys Cys Ala Val Met Ser Asp Arg Val Pro Asp Ser Ile  
85 90 95  
Val Lys Gly Thr Gly Thr Val Ala Arg Ser Arg Pro His Ser Pro Cys  
100 105 110  
Arg Gly His Trp Ala Cys His Gln Gly His Gly Tyr Gly Gly Ile Gly  
115 120 125  
Pro Thr Leu Thr Arg Pro Gln Ser Ala Pro Gly Leu Ser Ser Arg Thr  
130 135 140  
Arg Val Arg Trp Pro Arg Pro Arg Pro His Ser Ser Cys Arg Gly His  
145 150 155 160  
Trp Ala Ser Gly Arg His Gly Gly Leu Asp Gly His Asp Cys Ser Gly  
165 170 175  
Lys Ala Trp Ser Ala Phe Gln Thr Ala Leu Ile Pro Phe Pro Asn Leu  
180 185 190

Gly Cys Thr Ser Gly Ala Glu Ala Ser Leu Thr Cys Phe Leu Ser Leu  
                   195                                  200                                  205

Ser Arg Val Thr Asn Glu Arg Val His Ser Gly Val Leu Leu  
           210                                  215                                  220

<210> 9  
 <211> 30  
 <212> RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: An  
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<210> 10  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: An  
           artificially synthesized oligo(dT) primer  
           sequence

<400> 10  
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<210> 11  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: An  
           artificially synthesized primer sequence

<400> 11  
 agcatcgagt cggccttggt g 21

<210> 12  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: An  
           artificially synthesized primer sequence

<400> 12  
gcggctgaag acggcctatg t